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	in DNA Strand ssarv2 lib/6mers' file. nown at open reading frames.	FIGURE 4 Page 1 of 12
-il     -i		i ii xmnipsti bini mboi1-1
pst1 pvu11 ttb1114-2	_ _  _pst1 iii hindi sphi	
mbo11-2     mbo11-2     mbo11-1   bstx   mbo11-1   bstx   mbo11-1   bg111     mbo11-1   bg111     mbo11-1     mbo11-1	I=1	ava3 tthTIII1-2 ecor5 bstXI binI
binI pvu11 tthIII1-2	.5511=1  hpa1 aha111	int1-1-1-1- mboi1-1 ava3
kpni mboli-i lostx scal pvuli ava3	I	hIndiff mbo11-1
-nde1lavr2lavr2- sca1		T-
scal		
 m55ff=f-1	<sup> </sup> mbo11-1	msEII binI avr2

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Figure 4
Page 2 of 12

- 1 CTGGAAGGGCTAATTTGGTCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATCTACCACAC GACCTTCCCGATTAAACCAGGGTTTCTTCTGTTCTCTAGGAACTAGACACCTAGATGGTGTG 26 mbo11, 50 bin1,
- ACAAGGCTACTTCCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCACT TGTTCCGATGAAGGGACTAACCGTCTTAATGTGTGGTCCCGGTCCCTAGTCTATAGGTGA 107 bini, 113 ecors,
- 6ACCTTTGGATGGTGCTTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAAGAGGCCAA CTGGAAACCTACCACGAAGTTCGATCATGGTCAACTCGGTCTCTTCCATCTTCTCCGGTT
- 183 TGAAGGAGACAACAGCTTGTTACACCCTATGAGCCTGCATGGGATGGAGGACGCGGAACTTCCTCTTGTTGTCGAACAATGTGGGATACTCGGACGTACCCTCCTGCGCCT
- 6AAAGAAGTGTTAGTGTGGAGGTTTGACAGCAAACTAGCATTTCATCACATGGCCCGAGA CTTTCTTCACAATCACCCCCCAAACTGTCGTTTGATCGTAAAGTAGTGTACCGGGCTCT 296 ava1,
- GCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGCCGACGTAGGCCTCATGATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCG
- 363 TGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGTCCCTCAGATGC ACCCCTGAAAGGTCCCTCCGCACCGGACCCGCCCTGACCCCTCACCGCAGGGAGTCTACG
- TGCATATAAGCAGACTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGACGTATATTCGTCTGACGAAAAACGGACATGACCCAGAGAGACCAATCTGGTCTAGACTC
- 483 CCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTT GGACCCTCGAGAGACCGATTGATCCCTTGGGTGACGAATTCGGAGTTATTTCGAACGGAA. 488 sac1, 518 af111, 532 hind111,
- 603 GACCCTTTTAGTCAGTGTGGAAAAATCTCTAGCAGTGGCGCCCGAACAGGGACGCGAAAG CTGGGAAAATCAGTCACACCTTTTTAGAGATCGTCACCGCGGGCTTGTCCCTGCGCTTTC
- CGAAAGTAGAACCAGAGGAGCTCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCACAG GCTTTCATCTTGGTCTCCTCGAGAGAGCTGCGTCCTGAGCCGAACGACTTCGCGCGTGTC
  - 723 CAAGAGGCGAGGGGGGGGGGGGTGACTGGTGAGTACGCCAATTTTTGACTAGCGGAGGCTAGAAGGTTCTCCGCTCCCGCCGCCGCTGACCACTCATGCGGTTAAAAACTGATCGCCTCCGATCTTC

Figure 4
Page 3 of 12

- LysileargleuargProglyGlyLysLysLysTyrLysLeuLysHisileValTrpala AAAATTCGGTTAAGGCCAGGGGGAAAGAAAAATATAAGTTAAAACATATAGTATGGGCA TTTTAAGCCAATTCCGGTCCCCCTTTCTTTTTATATTCAATTTTGTATATCATACCCGT
- 903 SerArgGluLeuGluArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCys
  AGCAGGGAGCTAGAACGATTCGCAGTCAATCCTGGCCTGTTAGAAACATCAGAAGGCTGC
  TCGTCCCTCGATCTTGCTAAGCGTCAGTTAGGACCGGACAATCTTTGTAGTCTTCCGACG
  959 pst1,
- 963 ArgGinileLeuGlyGinLeuGinProSerLeuGinThrGlySerGluGluLeuArgSer AGACAAATATTGGGACAGCTACAGCCATCCCTTCAGACAGGATCAGAAGAACTTAGATCA TCTGTTTATAACCCTGTCGATGTCGGTAGGGAAGTCTGTCCTAGTCTTCTTGAATCTAGT 1002 bini, 1008 mbo11,
- LeuTyrAsnThrvalAlaThrLeuTyrCysValHis6lnArgIleAspValLysAspThr TTATATAATACAGTAGCAACCCTCTATTGTGTACATCAAAGGATAGATGTAAAAGACACC AATATATTATGTCATCGTTGGGAGATAACACATGTAGTTTCCTATCTACATTTTCTGTGG
- LysglualaLeugluLysilegluglugluglnAsnLysSerLysLysLysAlaglngln
  AAGGAAGCTTTAGAGAAGATAGAGGAAGGAAGACAAAACTAAGAAAAAGCCACAGCAA
  TTCCTTCGAAATCTCTTCTATCTCCTTCTCGTTTTTCATTCTTTTTCCGTGTCGTT

  1087 hind111, 1097 mbo11, 1107 mbo11, p25
- AlaAlaAlaAlaAlaGlyThr6lyAsnSerSerGlnValSerGlnAsnTyrProlleVal
  6CAGCAGCTGCAGCTGGCACAGGAAACAGCAGGCCAGGTCAGCCAAAATTACCCTATAGTG
  CGTCGTCGACGTCGACCGTGTCCTTTGTCGTCGGTCCAGTCGGTTTTAATGGGATATCAC
  1147 pvu11, 1150 pst1, 1153 pvu11, 1156 tthIII1,
- 6lnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerProArgThrLeuAsnAlaTrp CAGAACCTACAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATGCATGG GTCTTGGATGTCCCCGGTTACCATGTAGTCCGGTATAGTGGATCTTGAAATTTACGTACC 1250 aha111, 1255 ava3,
- VallysValValGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeu GTAAAAGTAGTAGAAAAAGGCTTTCAGCCCAGAAGTAATACCCATGTTTTCAGCATTA CATTTTCATCATCTTTTTCCGAAAGTCGGGTCTTCATTATGGGTACAAAAGTCGTAAT 1275 mbo11,
- SerGluglyAlaThrProGlnAspLeuAsnThrMetLeuAsnThrValGlyGlyHisGln
  TCAGAAGGAGCCACCCCCACAAGATTTAAACACCATGCTAAACACAGTTGGGGGGACATCAA
  AGTCTTCCTCGGTGGGGTGTTCTAAATTTGTGGTACGATTTGTGTCACCCCCCTGTAGTT
  1346 aha111,
- AlaalaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgVal GCAGCCATGCAAATGTTAAAAGAGACTATCAATGAGGAAGCTGCAGAATGGGATAGAGTG CGTCGGTACGTTTACAATTTTCTCTGATAGTTACTCCTTCGACGTCTTACCCTATCTCAC
- HisprovalHisAlaGlyProlleAlaProGlyGlnMetArgGluProArgGlySerAsp CATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAAATGAGAGAACCAAGGGGAAGTGAC GTAGGTCACGTACGTCCCGGATAACGTGGTCCGGTTTACTCTCTTTGGTTCCCCTTCACTG

- 1623 ATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAAGGAACCCTTTAGAGATTAAGACAAAGAACCAAAGGAACCCTTTAGAGATTAAGACAAAGACCAAAGGAACCCTTTAAGACAAAGAACCAAAGGAACCCTTTAAGAGATTAAGACATTTCTGTTCCTTGGGAAATCTCTAAAGACAAAGAACCTTAAAGACCTGTATTCTGTTCCTTGGGAAATCTCTAAAGACCTGTATTCTGTTCCTTGGGAAATCTCTAA
- TyrvalAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnAspValLysAsn TATGTAGACCGGTTCTATAAAACTCTAAGAGCCGAACAAGCTTCACAGGATGTAAAAAAT ATACATCTGGCCAAGATATTTTGAGATTCTCGGCTTGTTCGAAGTGTCCTACATTTTTTA 1720 hind111,

Figure 4 Page 4 of 12

- pMetThrGluThrLeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLys GATGACAGAAACCTTGTTGGTCCAAAATGCAAACCCAGATTGTAAGACTATTTTAAAA CTACTGTCTTTGGAACAACCAGGTTTTACGTTTGGGTCTAACATTCTGATAAAATTTT 1743 1796 aha111.
- 1803 1827 mbo11,
- 1863
- 1923
- GlyLysGluGlyHisIleAlaLysAsnCysArgAlaProArgLysLysGlyCysTr 1983 GGCAAAGAAGGGCACATAGCCAAAAATTGCAGGGCCCCTAGGAAAAATTGCAGGGCCCCCCTAGGAAAAATTGCAGGGGATCCTTTTTCCCGACAACCTCT 2014 apa1, 2019 avr2,
- 2043 2102 mbo11,
- LysileTrpProSerTyrLysGlyArgProGlyAsnPheLeuGlnSerArgProGluPro AAGATCTGGCCTTCCTACAAGGGAAGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCA TTCTAGACCGGAAGGATGTTCCCTTCCGGTCCCTTAAAAGAAGTCTCGTCTGGTCTCGGT 2104 bgl11, 2141 mbo11,
- ThralaproprogluGluSerPheArgPheGlyGluGluLysThrThrProSerGlnLys ACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGAAACAACTCCCTCTCAGAAG TGTCGGGGTGGTCTTCTCCCAAAGCCCCTCCTCTTTTGTTGAGGGAGAGTCTTC 2163 2175 mbo11.
- 61nGluProIleAspLysGluLeuTyrProLeuThrSerLeuArgSerLeuPheGlyAsn CAGGAGCCGATAGACAAGGAACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGCAAC GTCCTCGGCTATCTGTTCCTTGACATAGGAAATTGAAGGGAGTCTAGTGAGAAACCGTTG 2223
- ASPPROSERSERGINOC GACCCCTCGTCACAATAAGGATAGGGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGA CTGGGGAGCAGTGTTATTCCTATCCCCCCGTTGATTTCCTTCGAGATAATCTATGTCCT 2283
- 2342 ECAGATGATACAGTATTAGAAGAAATGAATTTGCCAGGAAAATGAAACCAAAAATGATA 2360 mbo11, 2375 bstXI,
- GlyGlyIleGlyGlyPheIleLysValArqGlnTyrAsp6lnIleProValGluIleCys GGGGGAATTGGAGGTTTTATCAAAGTAAGACAGTACGATCAGATACCTGTAGAAATCTGT CCCCCTTAACCTCCAAAATAGTTTCATTCTGTCATGCTAGTCTATGGACATCTTTAGACA 2402
- 2462 ĞĞÁCATAÄÄĞĞTÄTÄĞĞTACAĞTATTAĞTAĞĞÁCCTACACCTĞTCAACATAATTĞĞÂAĞÁ CCTGTATTTCGATATCCATGTCATAATCATCCTGGATGTGGACAGTTGTATTAACCTTCT 2517 mbo11,
- AsnleuleuThrGlnileGlyCysThrLeuAsnPheProIleSerProIleGluThrVal AATCTGTTGACTCAGATTGGTTGTACTTTAAATTTCCCCATTAGTCCTATTGAAACTGTA TTAGACAACTGAGTCTAACCAACATGAAATTTAAAGGGGTAATCAGGATAACTTTGACAT 2522 2548 aha111, 2577 tthIII1,
- ysleulysPro61yMetAsp61yProLysVallys61nTrpProLeuThr61u 2582 EGTCATTTTAATTTCGGTCCTTACCTACCGGGTTTTCAATTCGTTACCGGTAACTGTCTT 2627 ball, 2639 mboll,
- 2642

LysileglyProgluAsnProTyrAsnThrProValPheAlaIleLysLysAspSer
AAAATTGGGCCTGAAAATCCATACAATACTCCAGTATTTGCTATAAAGAAAAAAAGACAGT
TTTTAACCCGGACTTTTAGGTATGTTATGAGGTCATAAACGATATTTCTTTTTTCTGTCA
2759 scal,

- ThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrp
  TGATTTACCTCTTTTGATCATCTAAAGTCTCTTGAATTATTTTCTTGAGTTCTGAAGACCC

- 2943 CATTTACCATACCTAGTATAAACAATGAGACACCAGGGATTAGATATCAGTACAATGTGGGTAAAATGAGATATCAGTACAATGTGGGATAAATGTGGGATAAATGTGGGTACAATGTGGGTCCCTAATCTATAGTCATGTTACACCC
- LeuproginglyTrpLysglySerProalallePheGinSerSerMetThrLyslieLeu
  CTGCCACAGGGATGGAAAGGATCACCAGCAATATTCCAAAGTAGCATGACAAAAATCTTA
  GACGGTGTCCCTACCTTTCCTAGTGGTCGTTATAAGGTTTCATCGTACTGTTTTTAGAAT
  3003 tthiii1, 3006 bstxi, 3021 bini,
- ValGlySerAspLeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGlnHis GTAGGATCTGACTTAGAAATAGGGCAGCATAGAACAAAAATAGAGGAACTGAGACAGCAT CATCCTAGACTGAATCTTTATCCCGTCGTATCTTGTTTTTATCTCCTTGACTCTGTCGTA
- TrpMetGlyTyrGluLeuHisProAspLysTrpThrValGlnProIleMetLeuProGlu TGGATGGGTTATGAACTCCATCCTGATAAATGGACAGTACAGCCTATAATGCTGCCAGAA ACCTACCCAATACTTGAGGTAGGACTATTTACCTGTCATGTCGGATATTACGACGGTCTT
- 2303 LysaspserTrpThrvalAsnaspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSer TITCTGTCGACCTGACAGTTACTGTATGTCTTCAATCACCCTTTTAACTTGACAGTTACTGTCAATCACCCGTTCA 3308 pvu11,
- GINII ETYPAL AGIYIL ELYSVALLYSGINL EUCYSLYSL EUL EUAFGGIYTHPLYSALA GTCTAAATACGTCCCTAAATTAAAGCAGTTATTAAACTCCTTAGAGGAACCAAAGCA GTCTAAATACGTCCCTAATTTCGTCAATACATTTGAGGAATCTCCTTGGTTTCGT
- 3423 LeuThreluvalileProleuThrelueluAlaeluLeuGluLeuAlaeluAsnargelu
  GATTGTCTTCATTATGGTGATTGTCTTCTTCGTCTCGATCTTGACCGTCTTTTGTCCCTC
  3447 mbo11,
- 3483 IleLeuLysGluProValHisGluValTyrTyrAspProSerLysAspLeuValAlaGlu
  TAAGATTTTCTTGGTCATGTACTTCATATATATCTGGGTAGTTTTCTGAATCATCGTCTT
- 3543 IleGinLysGinGlyGinTrpThrTyrGinIleTyrGinGluProPheLysAsn
  TATGTCTTCGTCCCCGTTCCGGTTACCTGTATAGTTTAAAAATTTATCAAGAGCCATTTAAAAAT
  3594 aha111.
- 3603 LeulysthrglyLystyrAlaArgMetArgGlyAlaHisThrAsnAspVallysGlnLeu GACTTTTGTCCTTTCATACGTTCCTACTCCCCACGGGTGTGATACTACTTTTGTCAAT 3659 hpa1,

Figure 4
Page 5 of 1:

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Figure 4
Page 6 of 12

- Threlualavaleintysvalse. hreluserilevaliletrpelytysil. rolys
  ACAGAGGCAGTGCAAAAAGTATCCACAGAAAGCATAGTAATATGGGGAAAGATTCCTAAA
  TGTCTCCGTCACGTTTTTCATAGGTGTCTTTCGTATCATTATACCCCTTTCTAAGGATTT

- LeuGluLysGluProlleValGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArg
  TTAGAGAAAGAACCCATAGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAATAGG
  AATCTCTTTCTTGGGTATCATCCTCGTCTTTGAAAGATACATCTACCCCGTCGATTATCC
- 61uThrLysLeuGlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysValValSer GAGACTAAATTAGGAAAAGCAGGATATGTTACTGACAGAGGAAGACAAAAAGTTGTCTCC CTCTGATTTAATCCTTTTCGTCCTATACAATGACTGTCTCCCTTCTGTTTTTCAACAGAGG 3943 mbo11,
- IlealaaspThrThrAsnGlnLysThrGluLeuGlnAlaIleHisLeuAlaLeuGlnAspATAGCTGACACAAAATCAGAAGACTGAATTACAAGCAATTCATCTAGCTTTGCAGGATTATCGACTGTGTTGTTTTAGTCTTCTGACTTAATGTTCGTTAAGTAGATCGAAACGTCCTA
  3983 mbo11,
- SerGlyLeuGluValAsmileValThrAspSerGlmTyrAlaLeuGlyIleIleGlmAla TCGGGATTAGAAGTAAACATAGTAACAGACTCACAATATGCATTAGGAATCATTCAAGCA AGCCCTAATCTTCATTTGTATCATTGTCTGAGTGTTATACGTAATCCTTAGTAAGTTCGT 4060 ava3,
- 61nProAspLysSerGluSerGluLeuValSerGlnIleIleGluGlnLeuIleLysLys CAACCAGATAAGAGTGAATCAGAGTTAGTCAGTCAAATAATAGAGCAGTTAATAAAAAAG GTTGGTCTATTCTCACTTAGTCTCAATCAGTCAGTTTATTATCTCGTCAATTATTTTTTC
- 61uLysValTyrLeuAlaTrpValProAlaHisLysGlyIleGlyGlyAsnGluGlnVal 6AAAAGGTCTACCTGGCATGGGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTA CTTTTCCAGATGGACCGTACCCATGGTCGTGTTTTCCTTAACCTCCTTTACTTGTTCAT 4163 kpn1,
- 4203 AsplysleuValSerAlaGlyIleArigLysValLeuPheleuAsnGlyIleAsplysAla GATAAATTAGTCAGTGCTGGAATCAGGAAAGTACTATTTTTGAATGGAATAGATAAGGCC CTATTTAATCAGTCACGACCTTAGTCCTTŢCATGATAAAAACTTACCTTATCCGG 4232 scal,
- 61nGluGluHisGluLysTyrHisSerAsnTrpArgAlaMetAlaSerAspPheAsnLeu CAAGAAGAACATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAGTGATTTTAACCTG GTTCTTCTTGTACTCTTTATAGTGTCATTAACCTCTCGTTACCGATCACTAAAATTGGAC 4266 mbo11,
- Proprovalvalalatysglullevalalasercysasplyscysglnleutysglyglu CCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAA GGTGGACACTATTTACAGTCGATTTTCCTCTT 4352 pvu11.
- Alamethis61y61nValAspCysSerPro61y11eTrp61nLeuAspCysThrHisLeu
  GCCATGCATGGACAAGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTA
  CGGTACGTACCTGTTCATCTGACATCAGGTCCTTATACCGTTGATCTAACATGTGTAGAT
  4386 ava3, 4410 bstXI, 4439 xba1,
- GluGlyLysileIleLeuValAlaValHisValAlaSerGlyTyrIleGluAlaGluVal
  GAAGGAAAATTATCCTGGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTT
  CTTCCTTTTTAATAGGACCATCGTCAAGTACATCGGTCACCTATATATCTTCGTCTTCAA
  4497 xmn1.
- 4503 IleproAlaGluThr6lyGlnGluThrAlaTyrPheLauLeuLysLeuAlaGlyArgTrp
  ATTCCAGCAGAGACAGGGCAGGAAACAGCATATTTTCTCTTAAAATTAGCAGGAAGATGG
  TAAGGTCGTCTCTGTCCCGTCCTTTGTCGTATAAAAGAGAAATTTTAATCGTCCTTCTACC
  4555 mbo11, 4560 ball,

Pigare 4 Page 7 of 12

- ProvallysthrileHisthraspasnGlySerAsnPhethrSerThrThrvallysAla CCAGTAAAAACAATACATACAGACAATGCCAGCAATTTCACCAGTACTACGGTTAAAGGCC GGTCATTTTTGTTATGTATGTCTGTTACCGTCGTTAAAGTGGTCATGATGCCAATTCCGG 4605 scal,
- AlacystrptrpAlaGlyIleLysGlnGluPheGlyIleProTyrAsnProGlnSerGlnGCCTGTTGGTGGGCAGGGATCAAGCAGGAATTTGGCATTCCCTACAATCCCCAAAGTCAACCACCACCCCCTAGTTCGTCCTTAAACCGTAAGGGATGTTAGGGGTTTCAGTT
- 61yValValGluSerMetAsnAsnGluLeuLysLysIleIleGlyGlnValArgAspGln
  4683 GGAGTAGTAGAATCTATGAATAATGAATTAAAGAAAATTATAGGACAGGTAAGAGATCAG
  CCTCATCATCTTAGATACTTAATTTCTTTTAATATCCTGTCCATTCTCTAGTC
- AlaGluHisLeuLysThrAlaValGInMetAlaValPheIleHisAsnPheLysArgLys
  GCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAA
  CGACTTGTGGAATTCTGTCGTCATGTTTACCGTCATAAGTAGGTGTTAAAATTTTCTTTT
  4752 afl11, 4791 aha111,
- GlyGlyIleGlyGlyTyrSerAlaGlyGluArgIleValAspIleIleAlaThrAspIle
  -4803 GGGGGGATTGGGGGGATACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATA
  CCCCCCTAACCCCCTATGTCACGTCCCCTTTCTTATCATCTGTATTATCGTTGTCTGTAT
- GlnThrLysGluLeuGlnLysGlnIleThrLysIleGlnAsnPheArqValTyrTyrArq
  CAAACTAAAGAACTACAAAAGCAAATTACAAAAATTCAAAAATTTTCGGGTTTATTACAGG
  GTTTGATTTCTTGATGTTTTCGTTTTAATGTTTTTAAAAAGCCCAAATAATGTCC
- AspAsnLysAspProLeuTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAla
  GACAACAAGATCCCCTTTGGAAAGGACCAGCAAAGCTTCTCTGGAAAGGTGAAGGGGCA
  CTGTTGTTTCTAGGGGAAACCTTTCCTGGTCGTTTCGAAGAGACCTTTCCACTTCCCCGT
  4956 hind111,
- ValVallleGlnAspAsnSerAspIleLysValValProArgArgLysAlaLysIleIle
  GTAGTAATACAAGATAATAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAAATCATT
  CATCATTATGTTCTATTATCACTGTATTTTCATCACGGTTCTTCTTTTCGTTTTTAGTAA
  5023 mbo11,
- MetGluAsnArgTrpGlnValMetIleValTrpGlnValAspArgMetArgIle
  ArgAspTyrGlyLysGlnMetAlaGlyAspAspCysValAlaSerArgGlnAspGluAsp
  AGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGAT
  TCCCTAATACCTTTTGTCTACCGTCCACTACTACACACCCGTTCATCTGTCCTACTCCTA
- - Phetyrarghishistyrgluserthrhisproargvalsersergluvalhisile
    TTTTATAGACATCACTATGAAAGTACTCATCCAAGAGTAAGTTCAGAAGTACACATC
    AAAATATCTGTAGTGATACTTTCATGAGTAGGTTCTCATTCAAGTCTTCATGTGTAG
    5185 scal,
- ProleuglyAspAlaLysLeuVallleThrThrTyrTrpGlyLeuHisThrGlyGluArg CCCCTAGGGGATGCTAAATTGGTAATAACAACATATTGGGGTCTGCATACAGGAGAAAGA GGGATCCCCTACGATTTAACCATTATTGTTATAACCCCAGACGTATGTCCTCTTTCT 5223 avr2,
- 61uTrpHisLeuGlyGlnGlyValAlalleGluTrpArgLysLysLysTyrSerThrGln GAATGCATTTGGGCCAGGGAGTCGCCATAGAATGGAGGAAAAAGAAATATAGCACAAA CTTACCGTAAACCCGGTCCCTCAGCGGTATCTTACCTCCTTTTTCTTTATATCGTGTGTT
- ValasproglyLeuAlaAspGinLeuIleHisLeuHisTyrPheAspCysPheSerGlu
  5341 GTAGACCCTGGCCTAGCAGACCAACTAATTCATCTGCATTATTTTGATTGTTTTTCAGAA
  CATCTGGGACCGGATCGTCTGGTTGATTAAGTAGACGTAATAAAAACTAACAAAAAGTCTT
- SerAlaileLysAsnAlaileLeuGlyTyrArqValSerProArqCysGluTyrGlnAla TCTGCTATAAAAAATGCCATATTAGGATATAGAGTTAGTCCTAGGTGTGAATATCAAGCA AGACGATATTTTTTACGGTATAATCCTATATCTCAATCAGGATCCACACTTATAGTTCGT S440 avr2.
- 61yHisAsnLysValGlySerLeuGlnTyrLeuAlaLeuAlaLeuIleThrProLys
  66ACATAACAAGGTAGGATCTCTACAATACTTGGCACTAGCAGCATTAATAACACCAAAA
  CCTGTATTGTTCCATCCTAGAGATGTTATGAACCGTGATCGTCGTAATTATTGTGGTTTT
  5476 binl.

Figure 4

Page 8 of 12

## CONFIDENTIAL

LysThrLysProProLeuProSerValLysLysLeuThrGluAspArgTrpAsnLysPro
AAGACAAAGCCACCTTTGCCTAGTGTTAAGAAACTGACAGAGGATAGATGGAACAAGCCC
TTCTGTTTCGGTGGAAACGGATCACAATTCTTTGACTGTCTCCTATCTACCTTGTTCGGG

.6G .6G

- AGCTTAAGAGAGAAGCTGTTAGACATTTTCCTAGGCCATGGCTCCATAGCTTAGGACAAT TCGAATTCTCTCTGACAATCTGTAAAAAGGATCCGGTACCGAGGTATCGAATCCTGTTA 5643 af111, 5670 avr2, 5676 nco1,
- ATATCTATGAAACTTATGGGGATACTTGGGCAGGAGTGGAAGCCATAATAAGAATTCTGC
  TATAGATACTTTGAATACCCCTATGAACCCGTCCTCACCTTCGGTATTATTCTTAAGACG

  5752 ecof1.
- 5761 AACAACTECTETTTATTCATTTCAGAATTEGETGTCAACATAGCAGAATAGGCATTATTC
  TTETTGACGACAAATAAGTAAAGTCTTAACCCACAGTTETATCGTCTTATCCGTAATAAG
- AACAGAGGAGAGAAGAAGAAATGGAGCCAGTAGATCCTAATCTAGAGCCCTGGAAGCAT TTGTCTCCTCTCTTTCTTTACCTCGGTCATCTAGGATTAGATCTCGGGACCTTCGTA 5836 mbo11, 5862 xba1,
- CCAGGAAGTCAGCCTAGGACTGCTTGTAACAATTGCTATTGTAAAAAGTGTTGCTTTCAT GGTCCTTCAGTCGGATCCTGACGAACATTGTTAACGATAACATTTTTCACAACGAAAGTA 5893 avr2,
- TGCTACECGTGTTTCACAAGAAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGA ACGATGCGCACAAAGTGTTCTTTTCCGAATCCGTAGAGGATACCGTCCTTCTTCGCCTCT 5945 mlu1, 5988 mbo11,
- 6001 CAGCGACGAAGAGCTCCTCAGGACAGTCAGACTCATCAAGCTTCTCTATCAAAGCAGTAA GTCGCTGCTTCTCGAGGAGTCCTGTCAGTCTGAGTAGTTCGAAGAGATAGTTTCGTCATT 6008 mbo11, 6011 sac1, 6016 mstll, 6038 hind111,
- 6061 GTAGTAAATGTAATGCAATCTTTACAAATATTAGCAATAGTATCATTAGTAGTAGTAGCA CATCATTTACATTACGTTAGAAATGTTTATAATCGTTATCATAGTAATCATCATCGT
- ATAATAGCAATAGTTGTGTGGACCATAGTACTCATAGAATATAGGAAAATATTAAGACAA
  TATTATCGTTATCAACACACCCTGGTATCATGAGTATCTTATATCCTTTTATAATTCTGTT
  6147 8c21,
- AGAAAATAGACAGATTAATTGATAGAATAAGAGAAAAAGCAGAAGACAGTGGCAATGAAA
  TCTTTTATCTGTCTAATTAACTATCTTTTTTCGTCTTCTGTCACCGTTACTTT
  6222 mbo11,
- 4241 VallysglythrargargasntyrglnHisLeuTrpArgTrpGlythrLeuLeuGly GTGAAGGGACCAGGAGGAATTATCAGCACTTGTGGAGATGGGGCACCTTGCTCCTTGGG CACTTCCCCTGGTCCTCTTAATAGTCGTGAACACCTCTACCCCGTGGAACGAGGAACCC
- ATGTTGATGATCTGTAGTGCTACAGAAAATTGTGGGTCACAGTTTATTATGGAGTACCT
  TACAACTACTAGACATCACGATGTCTTTTTTAACACCCCAGTGTCAAATAATACCTCATGGA
- ValTrpLysGluAlaThrThrThrLeuPheCysAlaSerAspAlaArgAlaTyrAspThr GTGTGGAAAGAAGCAACTACCACTCTATTTTGTGCATCAGATGCTAGAGCATATGATACA CACACCTTTCTTCGTTGATGGTGAGATAAAACACGTAGTCTACGATCTCGTATACTATGT
- 61uValHisAsnValTrpAlaThrHisAlaCysValProThrAspProAsnProGlnGlu GAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCCAAGAA CTCCATGTATTACAAACCCGGTGTGTACGGACACATGGGTGTGGGGTTGGGGTGTACTA
- 4481 ValleuGlyAsnvalThrGluAshPheAsnMetTrpLysAsnAsnMetValGluGln
  GTAGTATTGGGAAATGTGACAGAAAATTTTAACATGTGGAAAAATAACATGGTAGAACAG
  CATCATAACCCTTTACACTGTCTTTTAAAATTGTACACCTTTTTATTGTACCATGTTGTACACTTTTTATTGTACCATGTTGTACACTTTTTATT
- ATGCAGGAGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAAATTAACCTACGTCCTCCTATATTAGTCAAATACCCTAGTTTCGGATTTCGGTACACATTTTAATTGG

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ProLeuCysValThrEeuAsnCysThrAspLeuGlyLysAlaThrAsnThrAsnSerSer CCACTCTGTGTTACTTTAAATTGCACTGATTTGGGGAAGGCTACTAATACCAATAGTAGT GGTGACAAACCCCTTCCGATGATTATGGTTATCATCA

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AshTrpLysGluGluIleLysGlyGluIleLysAshCysSerPheAshIleThrThrSer
AATTGGAAAGAAGAAAAAAAGGAGAAAATAAAAAACTGCTCTTTCAATATCACCACAAGC
TTAACCTTTCTTCTTTATTTTCCTCTTTATTTTTTGACGAGAAAGTTATAGTGGTGTTCG
6670 mbo11,

- ValileThrGlnAlaCysProLysValSerPheGluProlleProlleHisTyrCysThr GTCATTACACAGGCCTGTCCAAAGGTATCATTTGAGCCAATTCCCATACATTATTGTACC CAGTAATGTGTCCGGACAGGTTTCCATAGTAAACTCGGTTAAGGGTATGTAATAACATGG 6851 stu1,
- ProalaglyPhealalleLeuLysCysAsnAsnLysThrPheAsnGlyLysGlyProCys
  CCGGCTGGTTTTGCGATTCTAAAGTGTAATAAAACGTTCAATGGAAAAGGACCATGT
  GGCCGACCAAAACGCTAAGATTTCACATTATTTTTGCAAGTTACCTTTTCCTGGTACA
- ThrasnvalSerThrvalGlnCysThrHisGlyIleArgProIleValSerThrGlnLeu
  ACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAATAGTGTCAACTCAACTG
  TGTTTACAGTCGTGTCATGTTACATGTGTACCTTAATCCGGTTATCACAGTTGAGTTGAC
- 7021 LeuleuAsnGlySerLeuAlaGluGluGluValVallleArgSerAspAsnPheThrAsn CTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTCACGAAC GACAATTTACCGTCAGATCGTCTTCTTCTCCATCATTAATCTAGACTGTTAAAGTGCTTG 7042 mbo11, 7045 mbo11, 7060 bg111,
- AsnalaLysThrIleIleValGlnLeuAsnGluSerValAlaIleAsnCysThrArgPro
  AATGCTAAAACCATAATAGTACAGCTGAATGAATCTGTAGCAATTAACTGTACAAGACCC
  TTACGATTTTGGTATTATCATGTCGACTTACTTAGACATCGTTAATTGACATGTTCTGGG
  7102 pvu11,
- AsnasnasnThrargLysSerIleTyfIleGlyProGlyArgAlaPheHisThrThrGly
  AACAACAATACAAGAAAAAGTATCTATATAGGACCAGGGAGAGCATTTCATACAACAGA
  TTGTTGTTATGTTCTTTTTCATAGATATATCCTGGTCCCTCTCGTAAAGTATGTTGTCCT
  7199 mbo11,
- ThreugluglnileValLysLysLeuArgGluglnPheGlyAsnAsnLysThrlleVal
  ACTTTAGAACAGATAGTTAAAAAATTAAGAGAACAGTTTGGGAATAATAAAACAATAGTC
  TGAAATCTTGTCTATCAATTTTTTAATTCTCTTGTCAAACCCTTATTATTTTGTTATCAG
- 7321 PheasingInserserGlyGlyAspProGluIleValMetHisserPheasinCysArgGly
  AAATTAGTTAGGAGTCCTCCCCTGGGTCTTTAACATTCCAAAATTATTAGAGGT
  AAATTAGTTAGGAGTCCTCCCCTGGGTCTTTAACATTACGTGTCAAAATTAACATCTCCC
  7331 mstil.
- GluphePheTyrCysAsnThrThrGlnLeuPheAsnAsnThrTrpArgLeuAsnHisThr
  GAATTTTTCTACTGTAATACAACACAACTGTTTAATACATGGAGGTTAAATCACACT
  CTTAAAAAGATGACATTATGTTGTTGTTGACAAATTATTATGTACCTCCAATTTAGTGTGA
- 7501 MettrpgingluvalglyLysalaMettyralaProProIleGlyGlyGlnIleSercys
  ATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCCTCCCATTGGAGGACAAATTAGTTGT
  TACACCGTCCTTCATCCTTTTCGTTACATACGGGGAGGGTAACCTCCTGTTTAATCAACA
- 7561 SerserAsnileThrGlyLeuLeuLeuThrArgAspGlyGlyThrAsnValThrAsnAsp
  TCATCAAATATTACAGGGCTGCTATTAACAAGAGATGGTGGTACAAATGTAACTAATGAC
  AGTAGTTTATAATGTCCCGACGATAATTGTTCTCTACCACCATGTTTACATTGATTACTG

Figure 4
Page 9 of 12

- 7741 ValVal61nArg61uLysArgAlaVal61yIleVal61yAlaMetPheLeuGlyPheLeu GTGGTGCAGAGAGAAAAAGAGCAGTGGGAATAGTAGGAGCTATGTTCCTTGGGTTCTTG CACCACGTCTCTTTTTCTCGTCACCCTTATCATCCTCGATACAAGGAACCCAAGAAC
- 7801 GGAGCAGGAAGCACTATGGGCGCAGTGTCATTGACGCTGACGGTACAGGCCAGACAA
  CCTCGTCGTCCTTCGTGATACCCGCGTCACAGTAACTGCGACTGCCATGTCCGGTCTGTT
- 7861 LeuLeuSerGlyIleValGlnGlnGlnAsnAsnLeuLeuArgAlaIleGluAlaGlnGln
  TTATTGTCTGGTATAGTGCAACAGCAGCAGCAACAA
  AATAACAGACCATATCACGTTGTCGTCTTGTTAAACGACTCCCGATAACTCCGCGTTGTT
- 7921 HISLEULEUGINLEUTHTVAITTPGIYIIELYSGINLEUGINAIAATGVAILEUAIAVAI
  CATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTG
  GTAGACAACGTTGAGTGTCAGACCCCGTAGTTCGTCGAGGTCCGTTCTCAGGACCGACAC
- 7981 GIUATGTYTLBUATGASPGINGINLBULEUGIYIIBTTPGIYCYSSETGIYLYSLBUILB GAAAGATACCTAAGGGATCAACAGCTCCTAGGGATTTGGGGTTGCTCTGGAAAACTCATT CTTTCTATGGATTCCCTAGTTGTCGAGGATCCCTAAACCCCAACGAGACCTTTTGAGTAA 7989 BStII, 7995 bini, 8007 avr2,
- CysThrThrAlaValProTrpAsnAlaSerTrpSerAsnLysSerLeuGluAspIleTrp
  TGCACCACTGCTGTGCCTTGGAATGCTAGTTGGAGTAATAAATCTCTGGAAGACATTTGG
  ACGTGGTGACGACACGGAACCTTACGATCAACCTCATTATTTAGAGACCTTCTGTAAACC
  8089 mbo11,
- ThreuleuGluGerGlnAsnGlnGlnGluLysAsnGluGlnGluLeuLeuGluLeu
  ACCTTACTTGAAGAATCGCAGAACCAACAAGAAAAGAATGAACAAGAATTATTAGAATTG
  TGGAATGAACTTCTTAGCGTCTTGGTTGTTCTTACTTGTTCTTAATAATCTTAAC
  8170 mbo11,
- ASPLYSTIPALESELEUTIPASHTIPPHESEILETHIASHTIPLEUTIPTYILELYS
  GATAAGTGGGCAAGTTTGTGGAATTGGTTTAGCATAACAAACTGGCTGTGGTATATAAAG
  CTATTCACCCGTTCAAACACCTTAACCAAATCGTATTGTTTGACCGACACCATATATTTC
- B281 IlePheIleMetIleValGlyGlyLeuValGlyLeuArgIleValPheAlaValLeuSer TATAAGTATACTATCATCCTCCGAACCATCCAAATTCTTATCAAAAACGACACGAAAACGACACGAAACGACACGAAAACGACACGAAAACGACACGAAAACGACACGAAAACGACACGAAAACGACACGAAAACGACACGAAAACGACACGA
- 8341 IlevalasmarqvalarqginglytyrserProLeuSerPheGlmThrarqLeuProVal ATAGTGAATAGAGTTAGGCAGGGATACTCACCATTGTCATTTCAGACCCGCCTCCCAGTC TATCACTTATCTCAATCCGTCCCTATGAGTGGTAACAGTAAAGTCTGGGCGGAGGGTCAG 8400 aval,
- ArgservalargleuvalaspflyPheleualaleuIleTrpfluaspleuargSerleu AGATCCGTTCGATTAGTGGATGGATTCTTAGCACTTATCTGGGAAGATCTGCGGAGCCTG TCTAGGCAAGCTAATCACCTACCTAAGAATCGTGAATAGACCCTTCTAGACGCCTCGGAC 8503 mbo11, 8505 bg111,
- CysleuPheserTyrArgArgLeuArgAspleuLeuleuIleAlaAlaArgThrValGlu
  TGCCTCTTCAGCTACCGCCGCTTGAGAGACTTACTCTTGATTGCAGCGAGGACTGTGGAA
  ACGGAGAAGTCGATGGCGGCGAACTCTCTGAATGAGAACTAACGTCGCTCCTGACACCTT
  8525 mbo11,

Figure 4 Page 10 of 12

- BS81 IleLeuGlyHisArgGlyTrpG.\_AlaLeuLysTyrTrpTrpSerLeuLeuG.nTyrTrp
  ATTCTGGGGCACAGGGGGTGGGAAGCCCTCAAATATTGGTGGAGTCTCCTGCAGTATTGG
  TAAGACCCCGTGTCCCCCACCCTTCGGGAGTTTATAACCACCTCAGAGGACGTCATAACC
  8629 pst1,
- IleGingluLeuLysAsnSerAlaValSerTrpLeuAsnAlaThrAlaIleAlaValThr
  B641 ATTCAGGAACTAAAGAATAGTGCTGTTAGCTGGCTCAACGCCACAGCTATAGCAGTAACT
  TAAGTCCTTGATTCCTTATCACGACAATCGACCGAGTTGCGGTGTCGATATCGTCATTGA
- 61uGlyThrAspArqVallleGluValAlaGlnArqAlaTyrArqAlaIleLeuHislle 6AGGGGACAGATAGGGTTATAGAAGTAGCACAAAGAGCTTATAGAGCTATTCTCCACATA CTCCCCTGTCTATCCCAATATCTTCATCGTGTTTCTCGAATATCTCGATAAGAGGTGTAT
- HisargargileargGinGlyLeuGluargLeuLeuOC MetGlyGlyLysTrpSer CATAGAAGAATTAGACAGGGCTTGGAAAGGCTTTTGCTATAAGATGGGTGGCAAGTGGTCA GTATCTTCTTAATCTGTCCCGAACCTTTCCGAAAACGATATTCTACCCACCGTTCACCAGT 8765 mbo11,
- AlaGluproAlaAlaAspGlyValGlyAlaValSerArgAspLeuGluLysHisGlyAla
  GCTGAGCCAGCAGCAGATGGGGTGGGAGCAGTATCTCGAGACCTGGAAAAACATGGAGCA
  CGACTCGGTCGTCGTCTACCCCACCCTCGTCATAGAGCTCTGGACCTTTTTGTACCTCGT
  8883 tthIII1, 8916 avai xhoi,
- IleThrSerSerAsnThrAlaAlaThrAsnAlaAspCysAlaTrpLeuGluAlaGln
  - F1002 61uGluVal61yPheProValArgPro61nValProLeuArgProMetThrTyrLys
    GAGGAAGAGGTGGGTTTTCCAGTCAGACCTCAGGTACCTTTAAGACCAATGACTTACAAG
    CTCCTTCTCCACCCAAAAGGTCAGTCTGGAGTCCATGGAAATTCTGGTTACTGAATGTTC

    9005 mbo11, 9029 mstII, 9034 kpn1,

- TreadpheaseserlysleualapheHisHisHetalaargGluleuHisProGluTyr
  TGGAGGTTTGACAGCAAACTAGCATTTCATCACATGGCCCGAGAGCTGCATCCGGAGTAC
  ACCTCCAAACTGTCGTTTGATCGTAAAGTAGTGTACCGGGGCTCTCGACGTAGGCCTCATG
  9399 ava1, 9417 sca1,
- 9422 TACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGCTGGGGACTTTCCAGGGATGTTTCTGACAAGGTCCCTGAAAGGTCCCTGAAAGGTCCC

Figure 4
Page 11 of 12

7542 CTTTTTECCTETACTEGGTCTC' - GETTAGACCAGATCTEAGCCTGEGAEC. TCTEGC GAAAAACGGACATGACCCAGAGAGACCAATCTEGTCTAGACTCGGACCCTCGAGAGACCG

Figure 4 Page 12 of 12

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9662 TETECCCETCTETTETETEACTCTEGTAACTAGAGATCCCTCAGACCCTTTTAGTCAGTGACACGGGCAGACAACACACTGAGACCATTGATCTCTAGGGAGTCTGGGAAAATCAGTCAC 9722

TEGAAAAATCTCTAGCAG ACCTTTTTAGAGATCGTC

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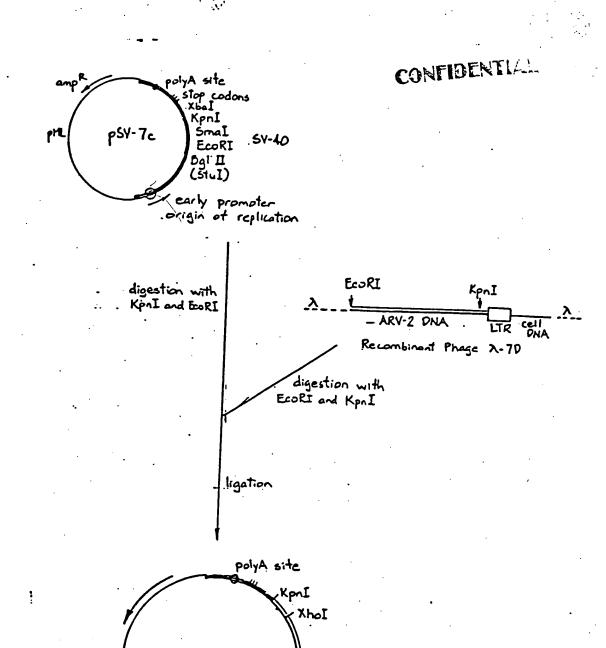
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FIGURE 5 4 of 4



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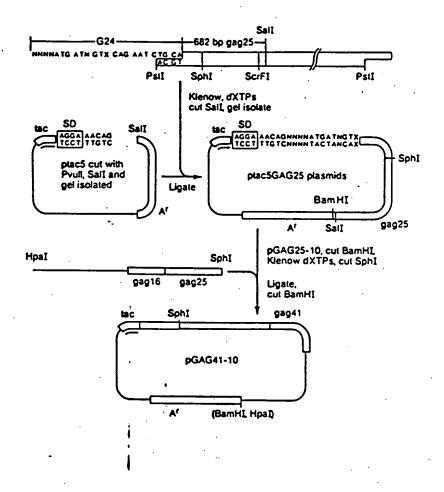
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Figure 7

CONFIDENCIA



# **FIG. 8**

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89	SOF GIUGIPAISTREPEGINASPLOVASHTRERLOVASHTREVAIGIFGIFGIFHISGINAISHARGINMOLLOVLYSGIUTRETIOASHGIWGIWAISAISGIUTEPASPAFFE 221 B teagaaggegeeceecearaagatttaarcaccatgetaarcacagggggggacatcaaggacaatgitaaagagactatcaatgaggagetgecaaatgggataaag	<b>.</b>
884	MISPLOYOIMISAIOGIPPLOIIGAIOPLOGIGIMPETALGIUPLOALGGIJSELASPIIGAIOGIJINLINLSOLINLIUGINGIUGIA IIOGIJILPNOLINLASAALADLO 261 Catclagiglaiglagggcetatiglaclaggccaatgagagaagggaagtgalascaggaaltaclagaaggaagaagaagaagaagaagaagaagaagaagaag	5
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## ARV GAG p16 - synthetic Parts A and B

Figure 10

- ArgGluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGlyLysIle AGAGAAGGTCACCAAATGAAGGACTGTACCGAAAGACAAGCTAACTTCTTGGGTAAGATC TCTCTTCCAGTGGTTTACTTCCTGACATGGCTTTCTGTTCGATTGAAGAACCCATTCTAG 129 bstE2, 131 hph, 148 rsaI, 161 alu1, 178 bgl11 xho2, 179 sau3a,

- ProlleAspLysGluLeuTyrProLeuThrSerLeuArgSerLeuPheGlyAsnAspPro CCAATCGACAAGGAATTGTACCCATTGACCTCTTTGAGATCCTTGTTCGGTAACGATCCC GGTTAGCTGTTCCTTAACATGGGTAACTGGAGAAACTCTAGGAACAAGCCATTGCTAGGG 307 taq1, 320 rsal, 331 mnl1, 339 xho2, 340 sau3a, 357 sau3a
- SerserGlnOP AM
  TCGAGCCAATGATAG
  AGCTCGGTTACTATCAGCT
  363 taq1, 377 acc1 hind11 sal1

= = LeuCysbelThrleudsnCysThraspleuGlyLysdleThrasnThrasnSerSerasnTrpLysGluGlulleLysGlyGlulleLysAsnCysSerPheAsnIleThrThrSerlle 171 Cicigigitacitiaaatigcactgattiggggaaggctaataataccaatagtagtagtiggaaagaagaagaagagagagaaataaaaaggcicitigaatatcaccacaaggata Argaiptysfleginlysglwarmiolouphoargainlouaspyolvolloaspasnaloserthrthrasmlyrthrasmlyrargloullomiscysarnargsorvol Agagaiaagaticagaaagaaaatgcactitttcgiaacctigaigtaccaatacataatgctactactactaccaactatacgataggigullomiscysaaraagatc llellegiyaspilearglysalemiscysasmileserargaiscintrpasmasmintleuginilevailyslyslewarggiuginphegiyasmasmlysihrilevaiphe 371 Ataataggagatataagaaagcacattgtaacattagaagcacaatggaataacactttagaacagntagaaaaattaagagaatagttgggaataatagagagtgttt 2 AsnVelserThrVelbinCysThrMisclyIleargrieIleVelserThrCinLeuleuleuasnblySerleualecleualecheslubiusIVellieArgserAsg Aatgicagcacagtacaatgtacacatgggattagggcaatagtgtgattaactggtgttaaatggcagtgtagcagaagaggtaattagatggaatttcacgaacaat 5 Ξ Velloubijanveithfeluasnpreanmettplysanasnretvoibiubigiubigespiopiesiesetloutpaspoimsolloutyspiolysvollyslouthf Gtattoscaaatotgaaaatttaacatotgaaaaataacatgetagaacagatgaaggaggatataatcagttatgggatgaagcctaagccatgtgtaaattaaccca Asneinserserstystyaspprestuttevalmermisserpheasncysargetystuppeppetyrcysasnthrthrethrempearanthrtrpargleubsmuss Aatcaatcetcassassesccassaattetaatscacaetttvaattetasassessaattittetactstaatacaactetttaataataatssassetaaatcacactsa giythelysgiyasrasptette ii oloupeopsafgii olysgirii oli oashmettipgi ngi utoi giysaloholtali opengijosi yelygi Ggarctaa ggaatgacacaatcatactcccatgia gaataa acaattataa acag ggagga ggaagtaga agagga agatagccctcccattga gaagtag Seraemileinteuteuthratgaspelyelythranvelthrandspihrelevelpheargpreelyelyasphelargaspasnirpargsereluleutyrlys Icaantatacaeeetiectatiaacaagastesteetaantetaactaateacaeeeeetticaeaeetegageagaagaagaagaaastaaaagteaattatahaa met Serarelleaspeys Seralethrelulysloutrpyelthryeltyrelyyetprevel atbitetada alcoal gtagtectacagaaaatteteegicacagittattategagtacetote PYK Terminator PYK Promoter Tyrlysvelitelysliediupreass Servel Ser Tataagtaataaaattgaccaaattgggtatct 1ga.

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TAACATGTEEAAAAATAACATEETAGAACAGATGCAGGGGTATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAAATTAACCCCA	LeudiytysaiothrasnthrasnSerasnTrpLysGiusiesjagiyGiysielysasnCysSerPheasnIiethrthrSerite 171 FigGGGAAGGCTACTAATACCAATAGTAGTAATTGGAAGAAGAATAAAGGAGAAATAAAAAGCTGCTGTTTGATATGACGCAGGCATA
	LewCysVelThrLewAsmCysThrAsplewGlyLysAleThrAsmThrAsmSerSerAsmTrp
O28	148 CTCIGIGITACTITAAATIGCACTGATTIGGGAAGGCIACTAATACCAATAGTAGTAGTAGTAGT

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6368	6508
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	33
6508 AATGICAGCACAGTACAATGAATTAGAATTAGACCAATAGIGTCAACTGATTAATGAATGAGAGAAGAAGAAGAAGAAGTAATTAGATTTGACGAACAATTTAGAATTTAGAAATTTAATTTAGAACAACAA	Alelysthrileilevelsnatussatuservelaleileasnaysthrafyreasnasnasnatuselysserileäyrregiyargiehemisthrihraiyary 331 6628 – Bataaaccataatagtacagagaatgaatagagaattaactgtacaacaacaatacaagaaagtacaagatatagagagag
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6748 ataatagaatataagaaaagcacattgtaacattagtagagcacaatggaatacacttagg	6868 — aatcaatcetabbacecabaaattetaatecacabttttaattetabbegebaatttttetactetaataacaactetttaataatalbegebegeteaa
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6989 GEACTAAAGEAATGACAATCATACTCCCATGTAGAATAA	Serasniie Tarbialeureureutargaspriyely tara Traaatattararrentertattaaraararrentertara
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PYK Terminator

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		•	COLUMN TO ELIA ELIA EL
Nickehide positions relative to. Figure 5		MetlleAspLysAlaGlnGluGluHi	is6luLysTyrHisSerAsnTrp
<b>FIGUR</b> 5	1	AGGXAACAG::::ATGAT:GA:AAGGCACAAGAAGAACA TCCXTTGTC:::TACTA:CT:TTCCGTGTTCTTCTTGT	ATRAGAAATATCACAGTAATT66
		32 mbo11, 38 nla111,	
3820	62	ArgalaMetAlaSerAspPheAsnLeuProProValVa AGAGCCATGGCTAGTGATTTTAACCTGCCACCTGTAGT TCTCGGTACCGATCACTAAAATTGGACGGTGGACATCA	I AGCAAAAGAAA I AG I AGCCAGC.
		66 nco1, 67 nla111, 118 nsp8II pvu11,	
<b>3880</b>	122	CysAspLysCysGlnLeuLysGlyGluAlaMetHisG TGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGC ACACTATTTACAGTCGATTTTCCTCTTCGGTACGTAC	CTGTTCATCTGACATCAGGTCCT
		135 alui, 151 nlaiii, 152 nsii ava3, 176 apyi bstXI ecorii scrFi,	155 nla111, 164 acc1, 1
3940	182	IleTrpGInLeuAspCysThrHisLeuGluGlyLysI ATATGGCAACTAGATTGTACACATCTAGAAGGAAAAA TATACCGTTGATCTAACATGTGTAGATCTTCCTTTTT	A   C   C   C   C   A   C   A   C   C
		198 rsaI, 205 xba1, 223 apy1 ecor11 se	·
4000	242	AlaSerGlyTyrIleGluAlaGluValIleProAlaG GCCAGTGGATATATAGAAGCAGAAGTTATTCCAGCAG CGGTCACCTATATATCTTCGTCTTCAATAAGGTCGTC	AGACAGGGCAGGAAACAGCAIAI
	•	263 xmn1,	
4060	302	PheLeuLeuLysLeuAlaGlyArgTrpProValLysTi TTTCTCTTAAAATTAGCAGGAAGATGGCCAGTAAAAA AAAGAGAATTTTAATCGTCCTTCTACCGGTCATTTTT	CAATACATACAGACAATGGCAGC
		321 mbo11, 326 bal1 cfr1 hae1, 327 ha	e111, 357 bbv fnu4h1,
4120	362	AsnPheThrSerThrThrValLysAlaAlaCysTrpT AATTTCACCAGTACTACGGTTAAGGCCGCCTGTTGGT TTAAAGTGGTCATGATGCCAATTCCGGCGGACAACCA	GGGCAGGGAICAAGCAGGAAIII
		366 hph, 371 scal, 372 rsal, 385 hae1 O5 binl, 406 dpn1 sau3a,	11, 386 fnu4h1 nsb11, 4
4180	422	61y11eProTyrAsnPro61nSerGlnGlyValVal6 66CATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAG CCGTAAGGGATGTTAGGGGTTTCAGTTCCTCATCATC	AATCTATGAATAATGAATTAAAG
		423 bsm1, 458 hinf1,	
4240	482	LysilelleGlyGlnValArgAspGlnAlaGluHisL AAAATTATAGGACAGGTAAGAGATCAGGCTGAACACC TTTTAATATCCTGTCCATTCTCTAGTCCGACTTGTGG	I I AAGACAGCAG I ACAAA I GOOD
	•	503 dpn1 sau3a, 518 afl11, 530 rsal,	
4300	542	ValPheileHisAsnPheLysArgLysGlyGlyIleG GTATTCATCCACAATTTTAAAAGAAAAGGGGGGATTG CATAAGTAGGTGTTAAAAATTTTCTTTTC	GGGGATACAGIGCAGGGGAAAGA
		547 fok1, 557 aha111,	; <u> </u>
4360	602	IlevalaspileilealathraspileGlnThrLysG ATAGTAGACATAATAGCAACAGACATACAAACTAAAG TATCATCTGTATTATCGTTGTCTGTATGTTTGATTTC	AACIACAAAAGCAAAIIACAAAA
		605 acc1,	
	662	IleGlnAsnPheArgValTyrTyrArgAspAsnLysA ATTÇAAAATTTTCGGGTTTATTACAGGGACAACAAAG	SPProLeuTrpLys61yProAla ATCCCCTTTGGAAAGGACCAGCA

Ayrò 722 LysteuleuirplysuivdiudiyalavalvallleginaspasnSerAspilelysvaí AAGCTTCTCTGGAAAGGTGAAGGGGCAGTAGTAATACAASATAATAGTGACATAAAAGTA TTCGAAGAGACCTTTCCACTTCCCCGTCATCATTATGTTCTATTATCACTGTATTTTCAT 722 hind111, 723 alu1, 737 hph.

ValproArgArgLysAlaLysIleIleArgAspTyr6lyLys6lnMetAlaGlyAspAsp
6TGCCAAGAAGAAAAGCAAAAATCATTAGGGATTATGGAAAACAGATGGCAGGTGATGAT
CACGGTTCTTCTTTTCGTTTTTAGTAATCCCTAATACCTTTTGTCTACCGTCCACTACTA
789 mbo11, 833 hph,

CysValAlaSerArgGlnAspGluAspAM
TGTGTGGCAAGTAGACAGGATGAGGATTAGTCGACGGAATTCTTTAGTAAAACACC
ACACACCGTTCATCTGTCCTACTCCTAATCAGCTGCCTTAAGAAATCATTTTGTGG

852 acc1, 859 fok1, 863 mnl1, 871 acc1 hind11 sal1, 872 taq1
, 878 ecor1,

FIGURE 12

2 of 2

ATG N-terminal domain gp120 C-terminal TAA domain

Fok-1 Bgi-2 Ava-1 Hga-1 gp41 Xho

lysargi

env-2

env-1

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env expression in yeast and bacteria

FIGURE 13

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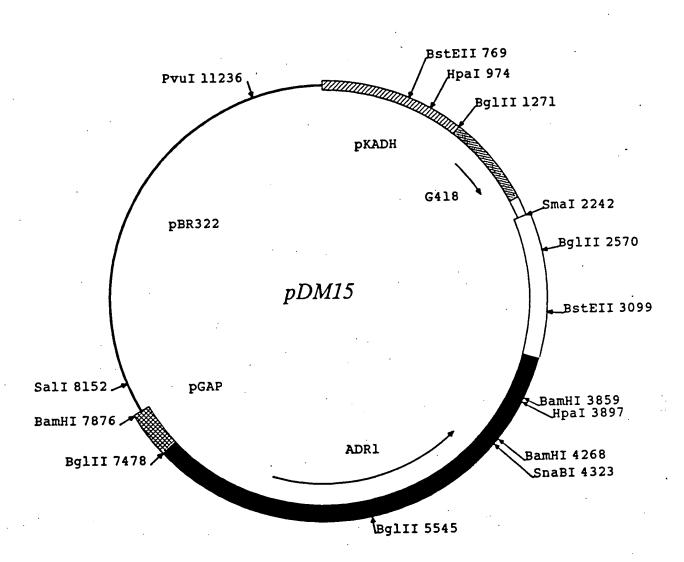


FIGURE 14

CONTECTATIVE

- GluGlyLeuHisGlyPheHisValHisGluPheGlyAspAspThrAlaGlyCysThrSer
  122 GAAGGCCTGCATGGATTCCATGTTCATGAGTTTGGAGATAATACAGCAGGCTGTACCAGT
  CTTCCGGACGTACCTAAGGTACAAAGTTACTCAAACCTCTATTATGTCGTCCGACATGGTCA
- Hisvalgiyaspleugiyasnvalthralaasplysaspgiyvalalaaspvalserile
  CATGTTGGAGACTTGGGCAATGTGACTGACAAAGATGGTGTGGCCGATGTGTCTATT
  GTACAACCTCTGAACCCGTTACACTGACGACTGTTTCTACCACACCGGCTACACAGATAA
- GluAspSerVallleSerLeuSerGlyAspHisCysIleIleGlyArgThrLeuValVal
  302 GAAGATTCTGTGATCTCACTCTCAGGAGACCATTGCATCATTGGCCGCACACTGGTGGTC
  CTTCTAAGACACTAGAGTGAGAGTCCTCTGGTAACGTAGTAACCGGCGTGTGACCACCAG
- HisGluLysAlaAspAspLeuGlyLysGlyGlyAsnGluGluSerThrLysThrGlyAsn
  CATGAAAAAGCAGATGACTTGGGCAAAGGTGGAAATGAAGAAAGTACAAAGACAGGAAAC
  GTACTTTTTCGTCTACTGAACCGGTTTCCACCTTTACTTCTTCATGTTTCTTGTCCTTTG

ENV 53
AlaGlySerArgLeuAlaCysGlyValIleGlyIleAlaMetAlaIleGluAlaGlnGln
GCTGGAAGTCGTTTGGCTTGTGTGTAATTGGGATCGCCATGGCTATCGAAGCTCAACAA
CGACCTTCAGCAAACCGAACACCACATTAACCCTAGCGGTACCGATAGCTTCGAGTTGTT

- HisleuleuGlmleuThrValTmpGlyIleLysGlmleuGlmAlaAmyValLeuAlaVal
  482 CACTTGCTGCAGTTGACCGTTTGGGGTATCAAGCAGTTGCAGGCTAGAGTTTTGGCTGTT
  GTGAACGACGTCAACTGGCAAACCCCATAGTTCGTCAACGTCCGATCTCAAAACCGACAA
- GluargtytleuargaspglugluleudeuglylletrigglyCysserglyLysleulle 542 GAAAGATACTTGAGAGATCAACAATTGTTGGGTATCTGGGGTTGTTCTGGTAAGTTGATT CTTTCTATGAACTCTCTAGTTGTTAACAACCCATAGACCCCAACAAGACCATTCAACTAA
- CysthrthralavalProtrpAsnalaSerTrpSerAsnLysSerLeuGluAspIleTrp
  602 TGTACCACCGCTGTTCCCTGGAACGCTTCTTGGTCTAACAAGTCTTTGGAAGACATCTGG
  ACATGGTGGCGACAAGGGACCTTGCGAAGAACCAGATTGTTCAGAAACCTTCTGTAGACC
- Aspasimentaltipmenglutipgluarggluileaspasity:Thrasothriletyr

  662 GACACATGACCTGGATGCAATGGGAAAGGAAATCGACAACTACACCAACACCATCTAC
  CTGTTGTACTGGACCTACGTTACCCTTTCTCTTTAGCTGTTGATGTGGTTGTGGTAGATG
- Asplystrphlaserleutrphsntrpheserllethrhsntrphy
  782 GACAGTGGGCAAGCTTGTGGAACTGGTTCTCTATCACCAACTGGTAG
  CTGTTCACCCGTTCGAACACCTTGACCAAGAGATAGTGGTTGACCATCAGCT

Translated Mol. Weight - 30414.22

FIGURE 15

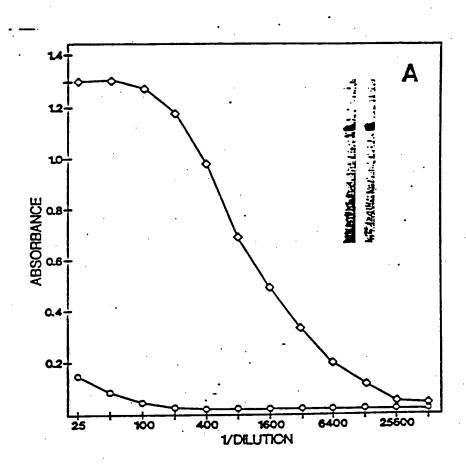


FIGURE 16



3 **\$** 

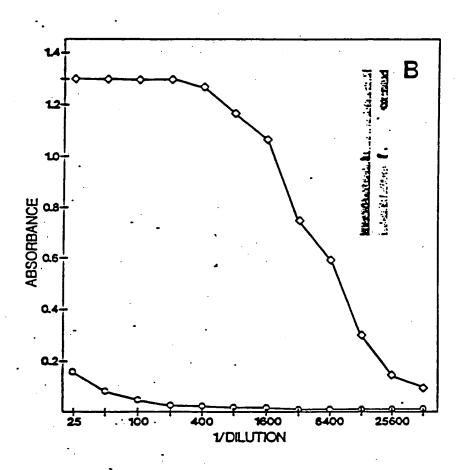


FIGURE 16

2 of 2

CORFEDENTIAL

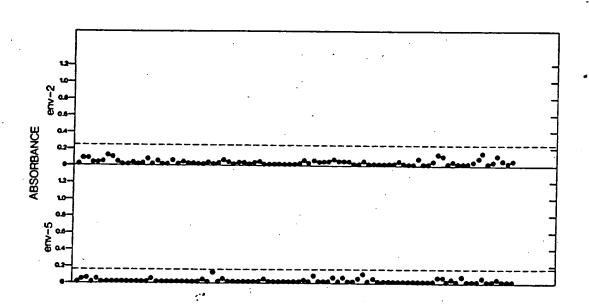


FIGURE 17

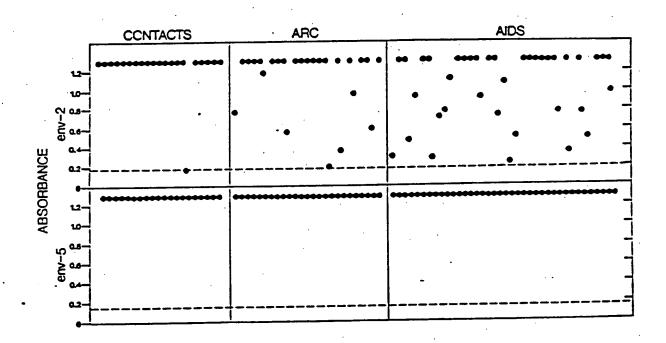
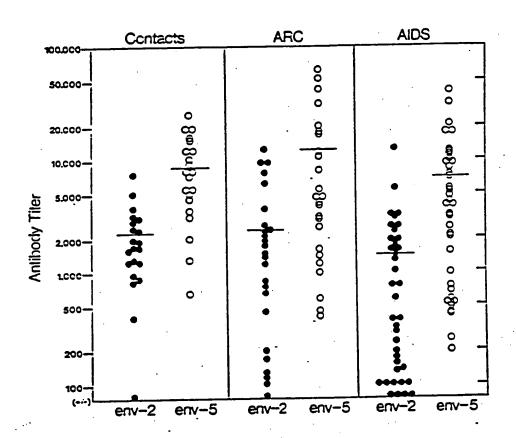


FIGURE 18



PIGURE 19

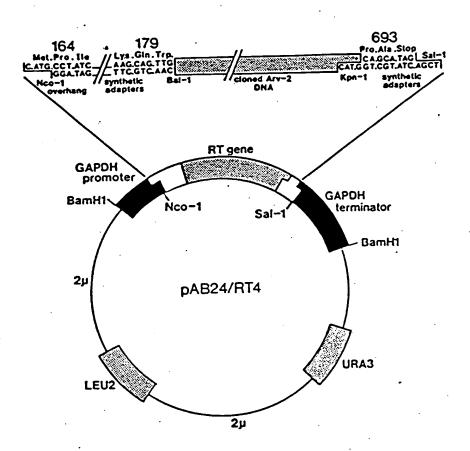


FIGURE 20

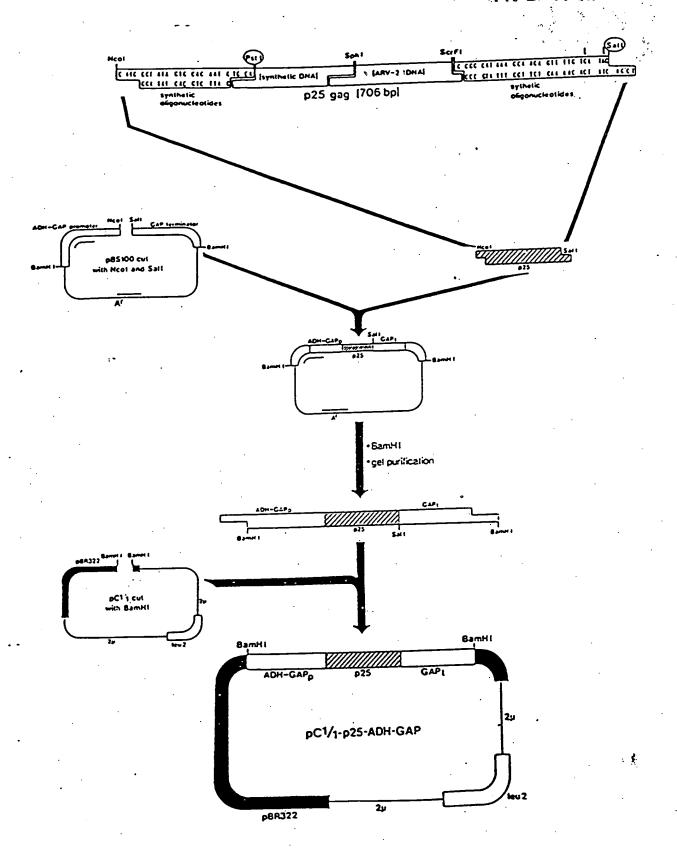


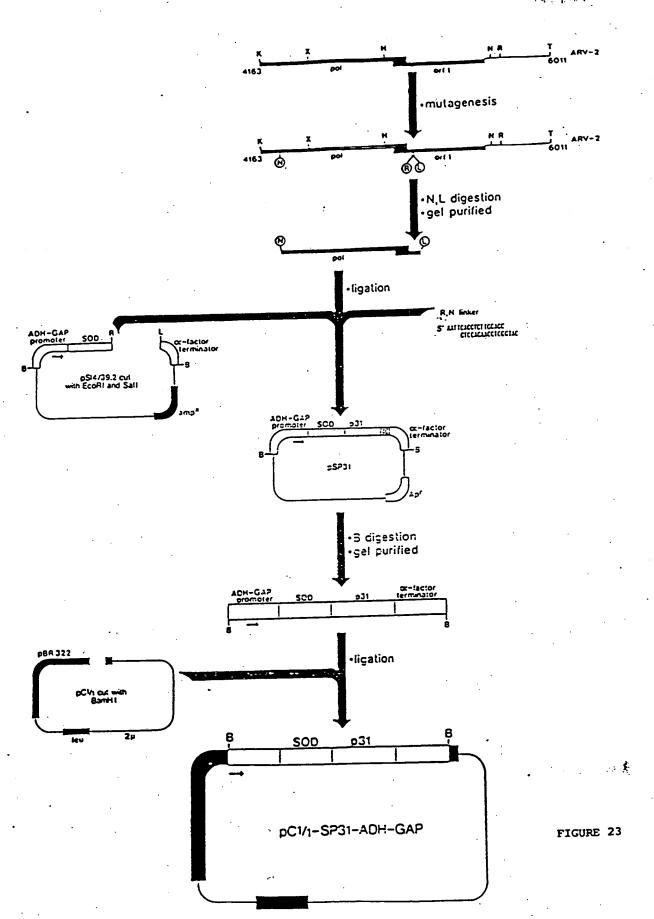
FIGURE 21



Ala lle Ser Pro Arg Thr Leu Ash Ala Trp Val Lys Val Val Glu GCC ATA TCA CCT AGA ACT TTA AAT GCT TGG GTA AAA GTA GTA GAA Ser Glu Gly Ala Thr Pro Gla Asp Leu Asn Thr Met Leu Asn Thr TCA GAA GGA GCC ACC CCT CAA GAT TTA AAC ACC ATG CTA AAC ACA ASA GIU GIU AIA AIA GIU TEP ASP AEG VAI HIS PED VAI HIS AIA AAT GAG GAG GCT GCC GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA 90
Giy Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp
GGG CCT ATT GCA CCA GGC CAA ATG AGA GAA CCA AGG GGA AGT GAC 110
Lie Ala Gly The The See The Leu Gla Glu Gla Ile Gly Tep Het
ATA GCA GGA ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG 120
The Ash Ash Ped Ped lle Ped Val Gly Glu Ile Tye Lys Arg Tep ACA AAT AAT CCA CCT ATC CCA GTA GGA GAA ATC TAT AAA AGA TGG 140
The file Leu Gly Leu Ash Lys file Val Ang Het Tyr Ser Pro Thrata ATC CTG GGA TTA AAT AAA ATA GTA AGA ATG TAT AGC CCT ACC 150 Ser the Leu Aso The Arg Glo Gly Pro Lys Glu Pro Phe Arg Asp AGC ATT CTG GAC ATA AGA CAA GGA CCA AAG GAA CCC TTT AGA GAT 170
Tyr Yal Asp arg Phe Tyr Lys Thr Lew Arg Ala Glw Glm Ala Ser TAT GTA GAC CGG TTC TAT AAA ACT CTA AGA GCC GAA CAA GCT TCA 190 Gin Asp Yai Lys Asn Trp Met Thr Giu Thr Leu Leu Yai Gin Asn CAG GAT GTA AAA AAT IGG ATG ACA GAA ACC TIG TIG GTC CAA AAT 200
Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala
AAC CCA GAT TGT AAG ACT ATT TTA AAA GCA TTG GGA CCA GCA Ala Thr Leu Glu Glu Net Met Thr Ala Cys Gla Gly Val Gly Gly GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT CAG GGA GTG GGG GGA

FIGURE 22

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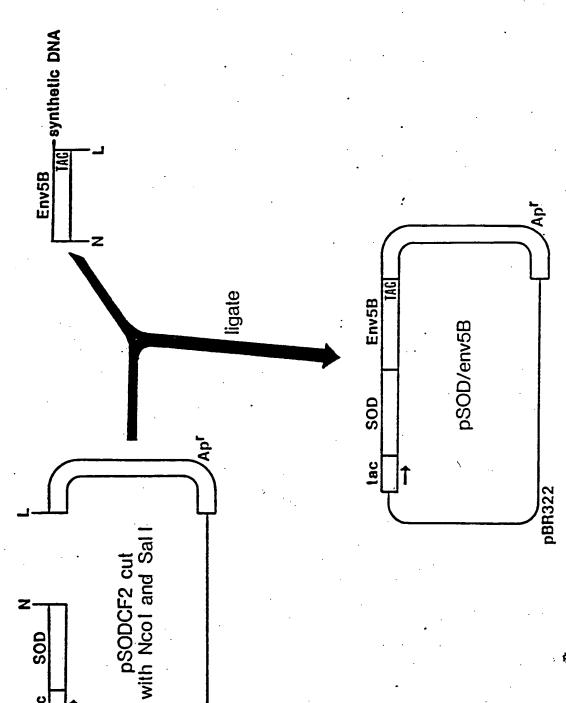


SOD -->
MetalaThrtysAla
ATGGCTACAAAGGCT
TACCGAIGTITCCGA

		•							· TACCGA	16111666
1363	6111	6161	TITE	LAGGGI	GAEGGE	CCCAST	TCAAGGT.	<b>ATTATTA</b>	CTTCGAG	61nLysGle Cagaaggae 67C11CC1
1443	AGTA	ATGG	ACCAC	SIGAAG	GIGIGO	GGGAAG	CATTAAA	GGACTGAC	TGAAGGC	Leuni eg 1 C1GCA1GG GACG1ACC1
1503	TICC	ATGT	TCATO	AGTTT	GGAGAI	TAATAC	AGCAGGC'	TGTACCAG	TGCAGGT	Francefin CC1CAC111 GGAG1GAA
1543	MATC	CTCT	ATCCA	MAAAA	CACGG1	GGGCC	AAAGGATI	GAAGAGAG	GCATGTT(	GlyAsplei GGAGACTIC CCTCTGAAC
1423	GGCA.	AT6T	GACTO	CTGAC	AAAGAT	GGTGT	GGCCGAT	GIGICTAT	TGAAGATI	Servalile ICTGTGAT( AGACACTA(
1683	TCAC	TCTC	AGGÁG	ACCAT	TĞCATC	ATTGG	CCGCACA	CTGGTGGT	CCATGAA	LYBALAAS AAAGCAGAI ITTCGTCIA
1743	GACT	7666	CAAAG	STEGA	AATGAA	GAAAG	TACAAAG	ACAGGAAA	CGCTGGA	Serargleu Agtcgtttg Tcagcaaa
1503	GCTTC	TGG	TGTAA	TTEGG	ATCGCC	GINAS	TTCAGGT	STIGGAGE	AMERALA!	931> Hetalaser Atggctag1 Taccgatca
1863	AspP: GATT:	TAA!	nL euf	rofro'	/alval Stagta	AlaLy	EGIUII#	/AIAIASe STAGCCAG	CTGTGAT	 LysCysG1# MAATGTCAG TTTACAGTG
1923	CTAA	نههد	AGAAG	CCATGO	ATGGA	CAAGTA	AGACTETA	AGTCCAGG	AATATGG	SINLOUAS P CAACTAGAT STIGATCIA
1983	TOTAC	ACA	TCTAG	AAGGAA	TTAKK	ATCCTO	SGTAGEAG	STICATGE.	AGCCAGTO	SIYTYFIIG GATATATA CTATATAT
2043.	GAAG	AGA	GTTA	TTCCAE	CAGAG	ACAGGO	CAGGAAA	CAGCATA	******	.eulysleu TTAAAATTA AATTTTAAT
2103	GCAGI	AAGA	<b>TGGC</b>	CAGTAA	MAAACA	ATACAT	TACAGACA	LATGGCAG:	CAATTICA	INCSECTNO ACCAGTACT IGGT CATGA
2163	ACSGT	TAAG	GCCG	CCTGTI	GGTGG	GCAGGG	SATCAAGO	AGGAATT	TGGCATT(	ProTyrasa CCTACAAT GGATGTTA
2223	CCCCA	AAGT	CAAG	EAGTAG	TAGAA	TCTATE	BAATAATG	MARTTANA	GAAAATTA	lleGlyGla NTAGGACAG NATCCTGTG
2263	GTAAG	AGAI	CAGG	CTEAAC	ACCTT	AAGACA	NGCAGTAC	CAAATGGC	AGTATTC/	LICHLSAST ATCCACAAT IAGGTGTTA
2343	TTTAA	AAGA	AAAG	GGGGGA	TTEGG	GGATAC	AGTECAG	66GAAAG	AATAGTAG	Asplielie Gacataata Etgtattai
2403	<b>GCAAC</b>	AGAC	ATAC	AAACTA	AAGAA	CTACAA	MAGCAAA	TTACAAA	AATT CAAA	ATTTTEG AATTTTEG TAAAAGC
5443	STTTA	TTAC	AGGG	ACAACA	AAGAT	CCCCTI	TGGAAAG	GACCAGC	MAAGETTO	eutrpLye TCTGGAAA AGACCTTI
2523	GGTGA	AGGG	GCAG'	TAGTAA	TACAA	GATAAT	AGTGACA	TAAAAGT	AGTGCCAA	AFQAFQLY1 AGAAGAAA ICTTCTTTT
2583	SCAAA	AATC	ATTA	GÉGATT	ATEGA	AAAEAE	ATGGCAG	GTGATGA	******	LI ASGRAPQ SCAAGTAGA SGTTCATCI
	ELAAS	061 u	A & D A	H						

CAGEATGAGGATTAG GTCCTACTCCTAATC

FIGURE 24



pBR322

tac

FIGURE 25

900 —>
Hetalaftirtysalavalcysvalizeutysdlykspolyfrovaldindlyileilean
Catoocokodakogocototocotoctoakogocokococokotocako
Coctocticoocokokogokoakoticococtocogokotokotokatika

Sequence of 500/env-

Phedludiniyadluserandiyproyaliyayalitrodyserilelyadiyleuthr Trodacadaaogaaactaatogaccactgaaggorogogogaocattaaaggactgact Aactogictitoctittoattaoctgotoactrocacocottogtaatttoctgactga

2

Gludiylərdi ədiyphətlisvaldi odlubhədiy həphatitaral adiycyəthicələr Garoocctocatocatocatoticatcatoratitisələrinin kacacasotistacator Cittoggacotroctaagoticaacticaaactotatitisisələri

122

AledlyProfilePheAenProLeuSerArgly#fileQlydlyProLyeAepgludluArg GCAGGTCCTCACTTTAATCCTCTATCCAGAAAACAGGGTGGGCCAAAGGATGAAGAGG CGTCCAGGAAGTGAAATTAGGAGATAGGTCTTTTGTGCCACCGGTTTCCTACTTCTCTCC

182

Higyaldiyaapleudiyanyaithiralahapiyakapdiyyalalahapyalserile Chiditodagacitogocantotoactoctoacaaagatostotococostototott Giacaactotoaacocottacactoacgactottotacacaccococtacacataa

252

GlubepSerValileSexLeuSerOlyhepHisCysileileGlyhrythrLeuValVal GAGGATTCTGTGATCTCACTCTCAGGAGACATTGCATCATTGGCGCCACTGTGACTGCTC CTTCTAAGACACTAGAGTGCTCTGGTAACGTAGTAACGGGGTGTGACCAG

302

362

AsphanPhethlabananalalyethetletletlatalantacheudangluservalalatie Gacaattycacgaacaatgasaaccataatagtacaactgaatgaatcheccaatt Ctottaaagtgctycytacgatytyggyattaytchgtcgactyactyrgchecytta

482

Abricyetherreptoranabarantherrepyaser i letyr i leglyreglyatyala Ametetrolagroccaacaacaatrolagaarahatretretrepsorocraggagacs tigacatottectrogettottetretretretretretratratratretregetectoetes

3

8

662

Env4 —>
AladlySerArgLeuNlaCysOlyVall1e0ly11eAlaHetGluValVall1eArgSer
GCTGGAAGTCGTTTGGCTTGTGGTGTAATTGGGATCGCCATGGAGTAGTAATTAGATCT
GGACCTTCAGCAACCGAACACACACATTAACCTTAGGGTACTAGATCTTAGT

122

| LysGln | Let | Lehan Hettrpd | Lysdl | Lysdln | Lysdln

## CONFIDENTIAL

Phelisther The Total of the Second Se

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Argicaulantiightelluglyfhrlysglyhanspfhrileileleutrocyskrylle
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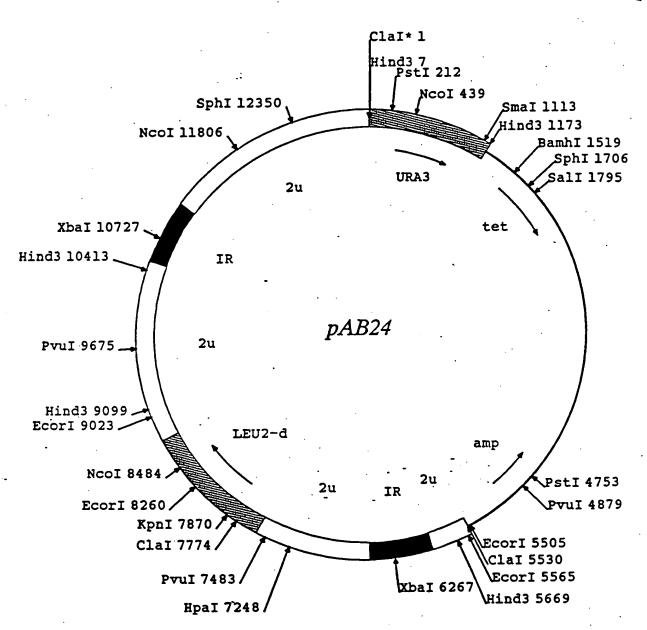


FIGURE 27

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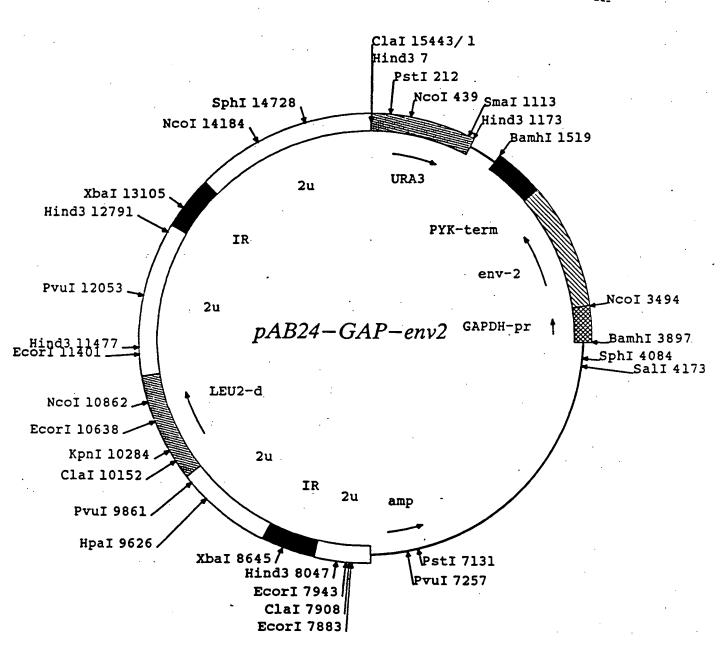


FIGURE 28

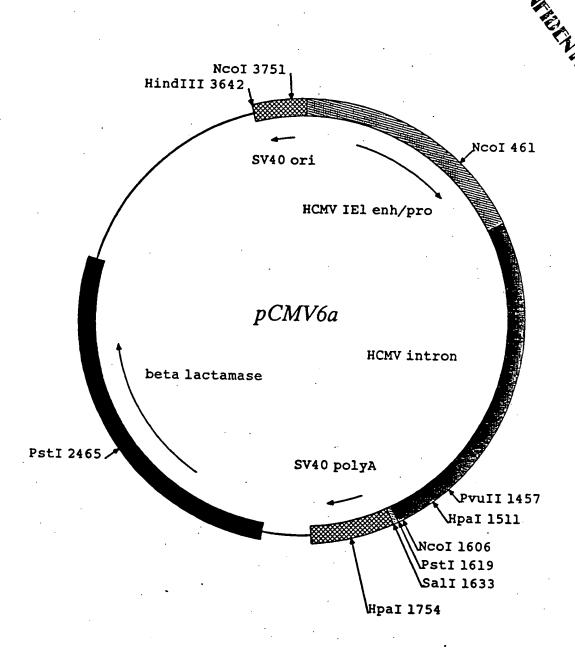


FIGURE 29



